## AMENDMENTS

**Listing of Claims**

The following listing of claims replaces all previous listings or versions thereof:

1-43. (Canceled)

44. (Currently amended) A method of assessing protein ~~stability,~~ folding and/or solubility comprising:

a) expressing in a host cell a fusion protein comprising (i) a protein of interest and (ii) a first segment of a marker protein, wherein said first segment has only ~~systemic~~systematic effects on the ~~stability,~~ folding and/or solubility of the protein of interest;

b) contacting said fusion protein produced in step a) with a second segment of said marker protein, wherein said second segment is capable of structural complementation with said first segment; and

c) determining structural complementation,

wherein a greater degree of structural complementation, as compared to structural complementation observed with appropriate negative controls, indicates ~~stability,~~ proper folding and/or solubility of said protein of interest.

45. (Previously presented) The method of claim 44, wherein said fusion is C-terminal to said protein of interest.

46. (Previously presented) The method of claim 44, wherein said fusion is N-terminal to said protein of interest.

47. (Previously presented) The method of claim 44, wherein said marker protein is selected from the group consisting of a target binding protein, an enzyme, a protein inhibitor, a fluorophore and a chromophore.

48. (Previously presented) The method of claim 47, wherein said marker protein is a target binding protein.

49. (Previously presented) The method of claim 48, wherein said target binding protein is ubiquitin.

50. (Currently amended) The method of claim 47, wherein said marker protein [[is]]comprises a chromophore.

51. (Currently amended) The method of claim 50, wherein said ~~chromophore~~marker protein is green fluorescent protein, blue fluorescent protein, yellow fluorescent protein, ~~luciferase~~ or aquorin.

52. (Previously presented) The method of claim 47, wherein said marker protein is an enzyme.

53. (Currently amended) The method of claim 52, wherein said enzyme is β-galactosidase, ~~cytochrome c, chymotrypsin inhibitor~~, luciferase, Rnase, phosphoglycerate kinase, invertase, staphylococcal nuclease, thioredoxin C, lactose permease, amino acyl tRNA synthase, ~~and~~or dihydrofolate reductase.

54. (Previously presented) The method of claim 53, wherein said enzyme is β-galactosidase.

55. (Previously presented) The method of claim 54, wherein said first segment is the α-peptide of β-galactosidase, and said second segment is the ω-peptide of β-galactosidase.

56. (Currently amended) The method of claim 44, wherein said protein of interest is Alzheimer's amyloid peptide (Aβ), SOD1, ~~presenillin~~presenilin 1 ~~and~~or 2, α-synuclein, amyloid A, amyloid P, CFTR, transthyretin, amylin, lysozyme, gelsolin, p53, rhodopsin, insulin, insulin receptor, fibrillin, α-ketoacid dehydrogenase, collagen, keratin, PRNP,

immunoglobulin light chain, atrial natriuretic peptide, seminal vesicle exocrine protein, β2-microglobulin, PrP, precalcitonin, ataxin 1, ataxin 2, ataxin 3, ataxin 6, ataxin 7, huntingtin, androgen receptor, CREB-binding protein, dentaorubral pallidoluysian atrophy-associated protein, maltose-binding protein, ABC transporter, glutathione S transferase, ~~and~~or thioredoxin.

57. (Previously presented) The method of claim 44, wherein said negative control utilizes a fusion protein that is improperly folded and/or insoluble.

58. (New) The method of claim 47, wherein said marker protein is cytochrome C or chymotrypsin inhibitor.